

Substitute the paragraph beginning on page 55, line 23, with the following paragraph:

By "agonist" is intended naturally occurring and synthetic compounds capable of enhancing one or more activity of the ET2 and/or GABRE receptor subunit. Such agonists include modified forms of the ET2 or GABRE polypeptide and agents which increase expression of ET2 and/or GABRE receptor subunits. By "agonistic activity" is intended the enhancement of one or more ET2 and/or GABRE receptor subunit activities. By "antagonist" is intended naturally occurring and synthetic compounds capable of inhibiting one or more activities of the ET2 and/or GABRE receptor subunit. Such antagonists include modified forms of the ET2 or GABRE polypeptide and agents which decrease expression of ET2 and/or GABRE receptor subunits. By "antagonistic activity" is intended the inhibition of one or more ET2 and/or GABRE receptor subunit activities. Whether any candidate "agonist" or "antagonist" of the present invention can enhance or inhibit ET2 and/or GABRE receptor subunit activity can be determined using art-known assays, including those described in more detail below.

In the Claims:

Please substitute the following claims 95, 98, 101, 104, 115 and 117 for the pending claims 95, 98, 101, 104, 115 and 117:

E6 Subj G1 Subj
95. (twice amended) An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to amino acids 1 to 260 of SEQ ID NO:42;

E6
Cont

wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 260 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 260 of SEQ ID NO:42.

E7

Sub G2 Sub 2 98. (twice amended) The isolated polynucleotide of claim 95, wherein said amino acid sequence is at least 95% identical to amino acids 1 to 488 of SEQ ID NO:42; wherein % identity is determined with parameters that calculate % identity over the full length of amino acids 1 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids 1 to 488 of SEQ ID NO:42.

E8

Sub G3 Sub 3 101. (twice amended) The isolated polynucleotide of claim 98, wherein said amino acid sequence is at least 95% identical to amino acids -17 to 488 of SEQ ID NO:42; wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -17 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -17 to 488 of SEQ ID NO:42.

E9

Sub G4 Sub 4 104. (twice amended) The isolated polynucleotide of claim 101, wherein said amino acid sequence is at least 95% identical to amino acids -18 to 488 of SEQ ID NO:42; wherein % identity is determined with parameters that calculate % identity over the full length of amino acids -18 to 488 of SEQ ID NO:42 and that allow gaps of up to 5% of the total number of amino acid residues in amino acids -18 to 488 of SEQ ID NO:42.

Sur G5 Sur 15 (twice amended) An isolated polynucleotide comprising a nucleotide sequence encoding an amino acid sequence at least 95% identical to the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642,
E10 wherein % identity is determined with parameters that calculate % identity over the full length of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the mature amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.

Sur G6 Sur 16 (twice amended) The isolated polynucleotide of claim 115, wherein said amino acid sequence is at least 95% identical to the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642;
E11 wherein % identity is determined with parameters that calculate % identity over the full length of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642 and that allow gaps of up to 5% of the total number of amino acid residues of the complete amino acid sequence encoded by the cDNA clone in ATCC Deposit No. 209642.